

FIG. 1

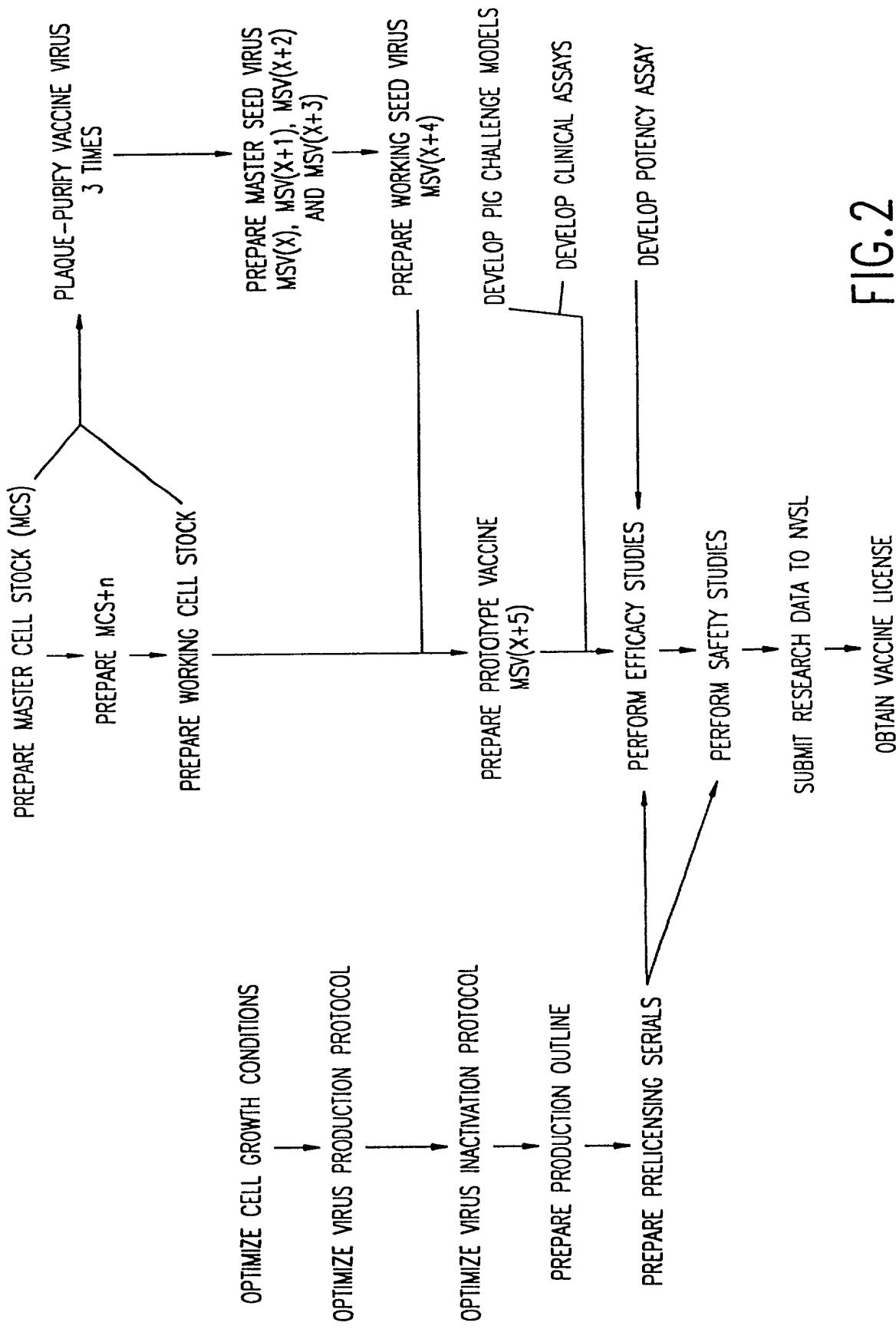


FIG. 2

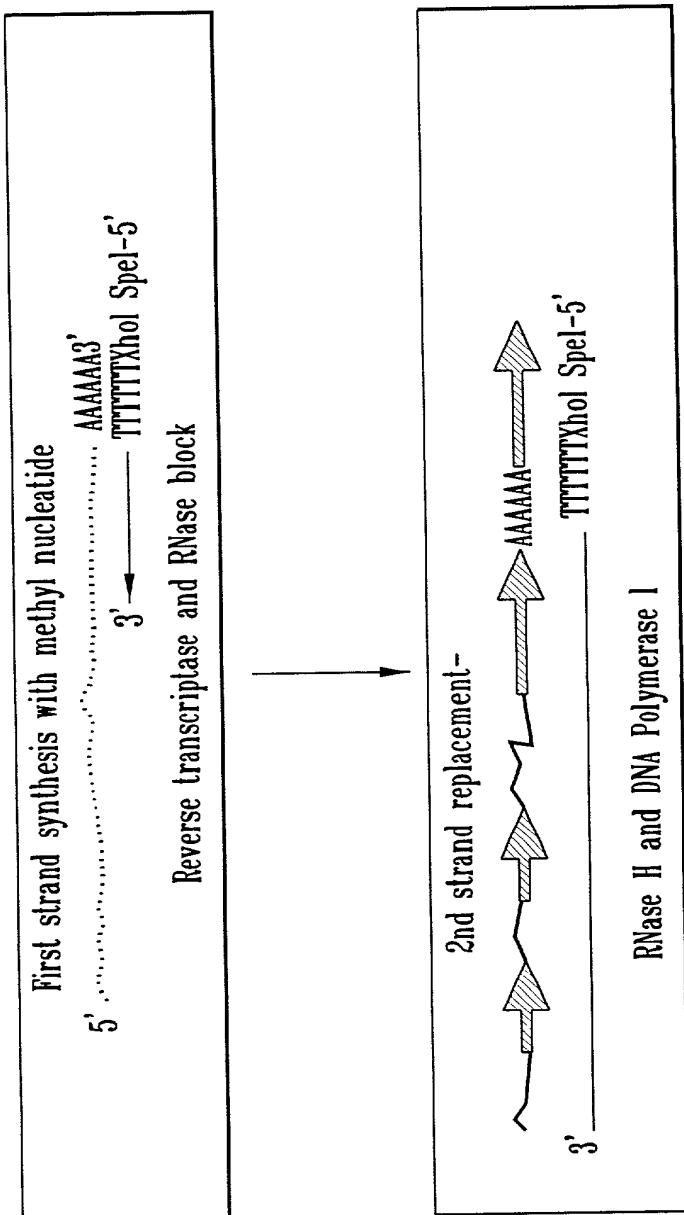


FIG. 3A

To Fig. 3b

From Fig.3a

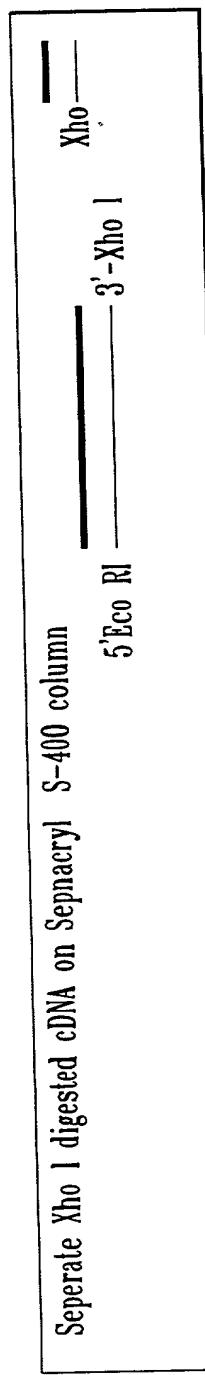
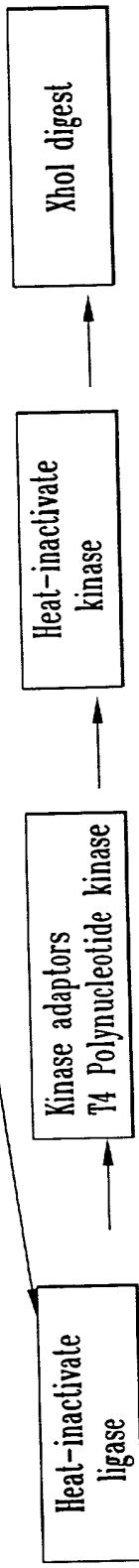
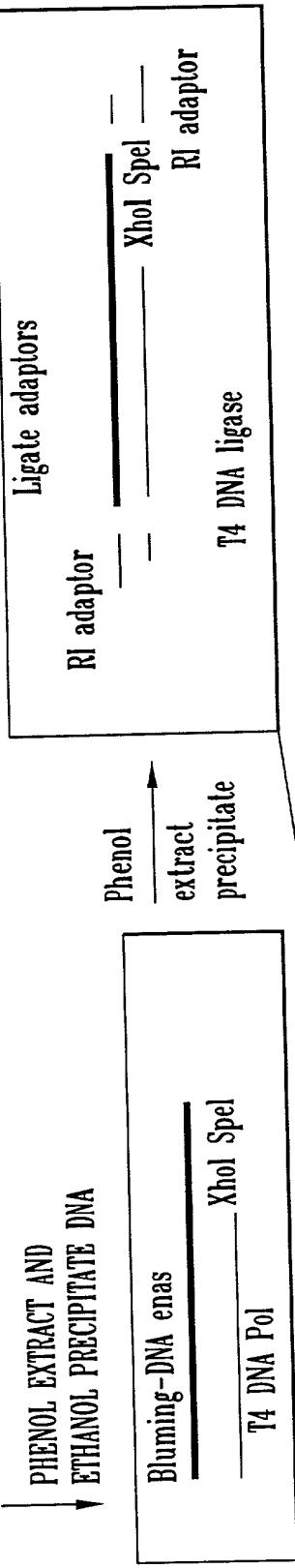
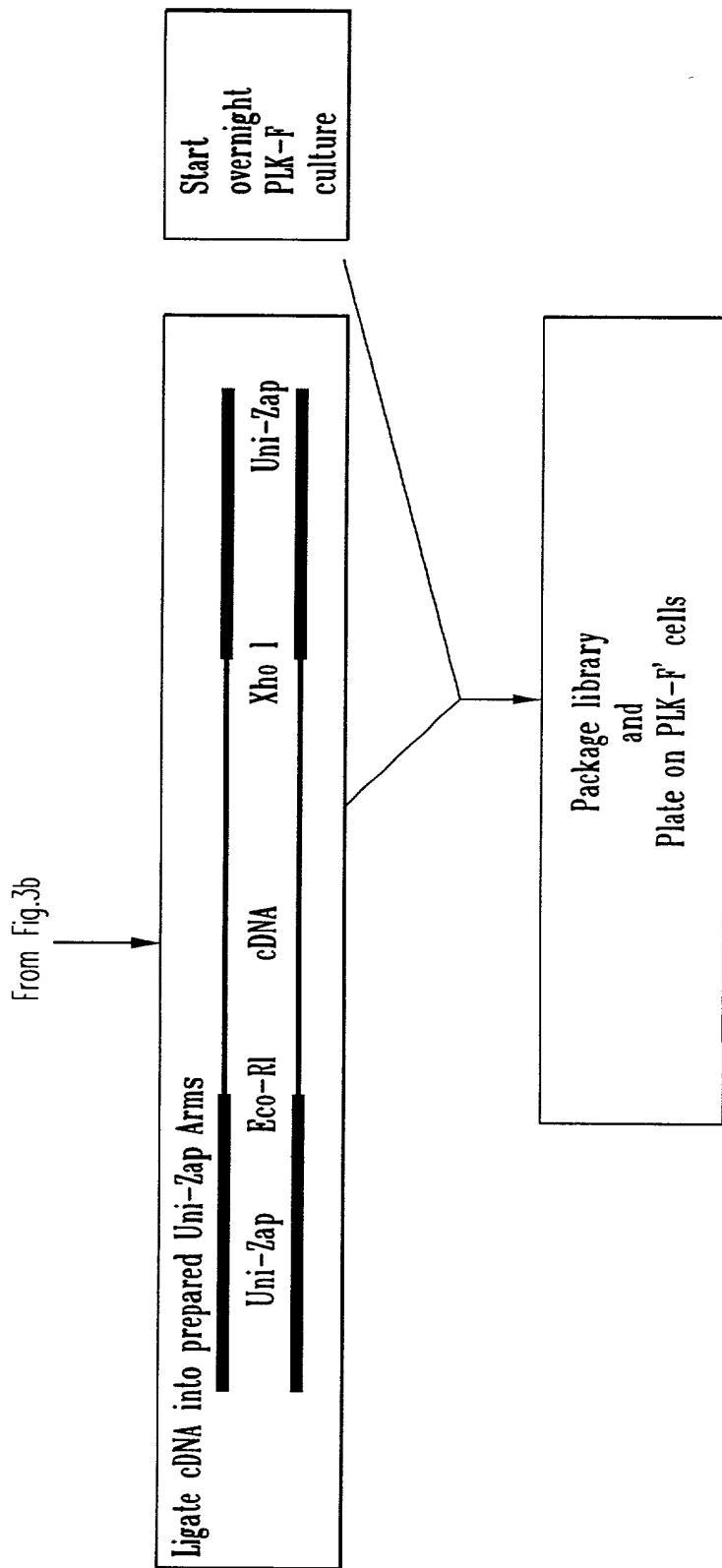


FIG. 3B

To Fig.3c

FIG. 3c



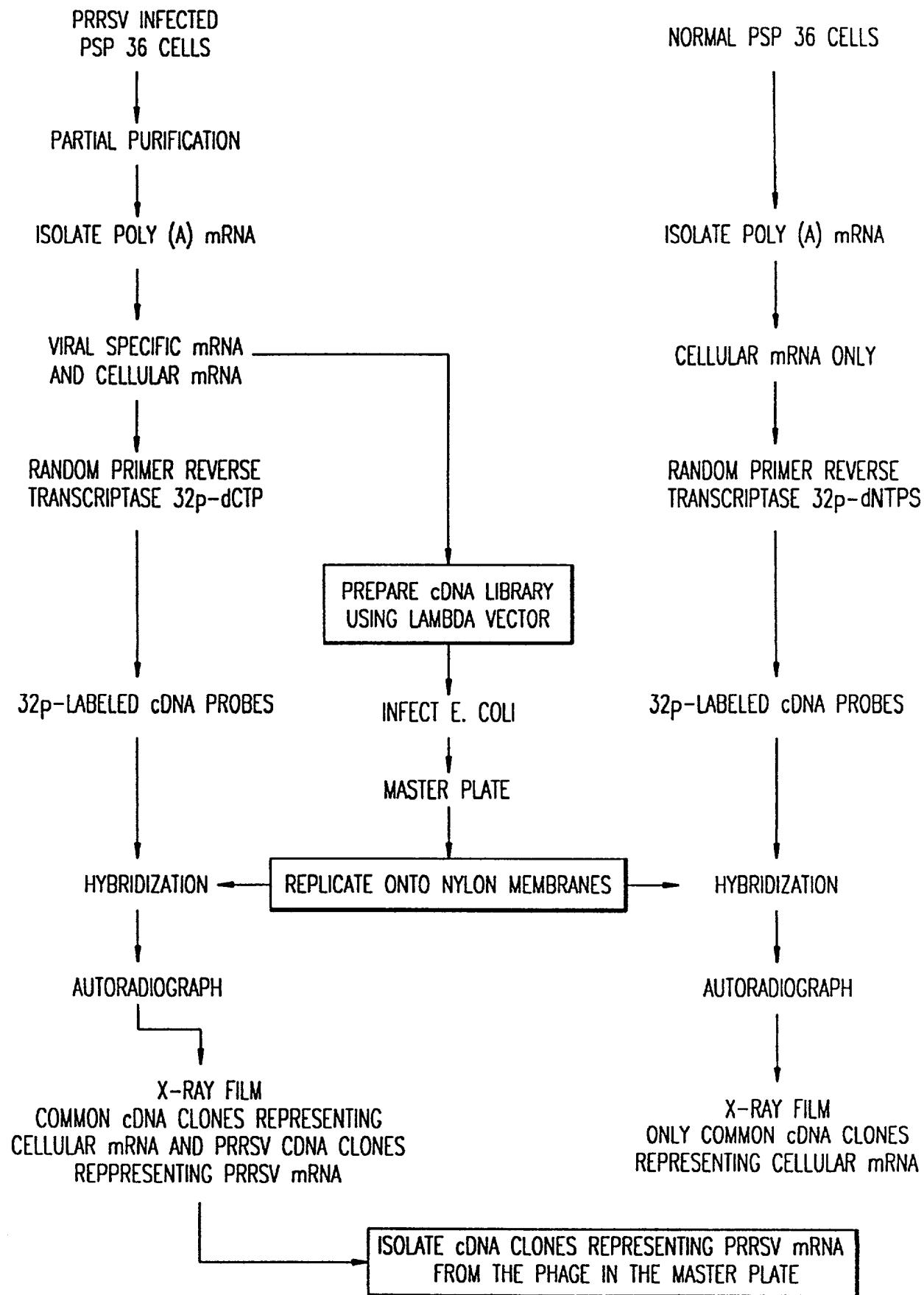


FIG.4

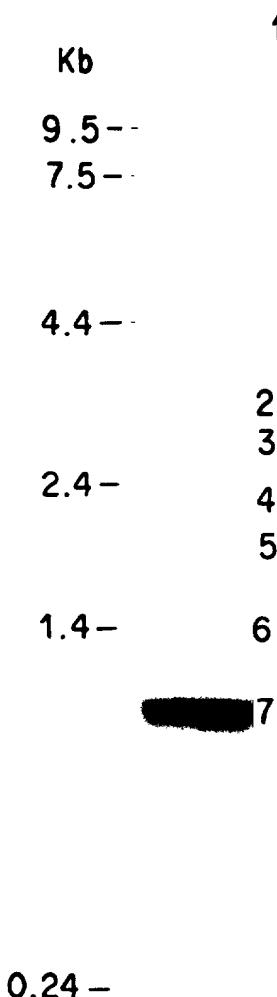


FIG.5

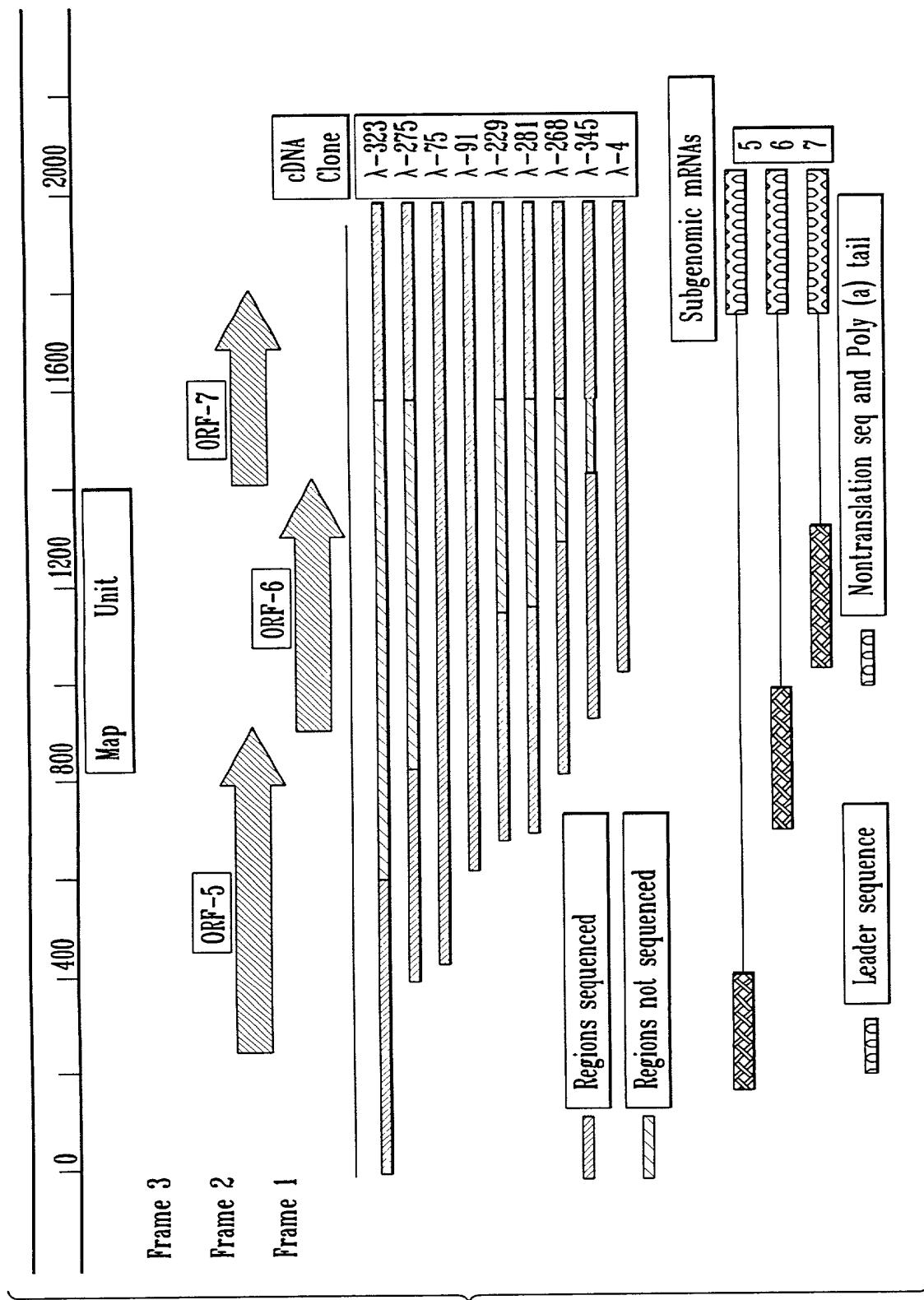


FIG. 6

100	GGCAGGCCCTTGCCTCCAAGACATCAAGTGCCTTAGGCATCGCAACTCGGCCCTGAGGCATTGCGAACAGTCCCTAGTGCCTACGGCATAAGG	
200	ACACCCGTGATAACTGTCACAGCCAAATTGTTACCGATGAGAATTATTGCAATTCTCTGATCTCTCATGCTTCTCTGCTTCTATGCTTCTCTG	
300	AGATGAGTGAAAAGGGATTAAAGGTGGTATTGGCAATGTGTCAAGGCATCGGGAGTGTGCCTCAACTTACAGTCAACATGTCAAGGAATT	
400	TACCCAACTGTTCTGGTAGTTGACCATGTGGCTGCCATTCAATGACGCCGAGACCATGAGGTGGCAACTGTTAGCCTGCTTTGGCATT	
400	DRF4 stop	
400	*** +1>DRF5 start	
500	CTGGGCAATTGAATGTTAAGTATGTTGGGAAATTGCTTGACCGGGCTGTTGCTCGAATTGCTTTTTGTTGTTATCGTGCCTGCTTGT	
600	GTTGGCTCGTACGGCCACGGAACAGGGCTCAAATTACAGCTGATTACAACCTGACGCTATGTGAGCTGAAATGGCACAGATTGGCTAGCTAATA	
700	AATTGACTGGCAGTGGAGTGGTTGCAATTTCCTGTTGACTCACATTGTCCTACACTAGCCATTCTTGACACAGTCGG	
700	TCTGGTCACTGTCACCGCTGGTTGCTACGGGGTATGTTCTGAGTAGCATGACGGGCTGTCGGCTGGCTGGCTGCGTGAATTGCTTCGTCAT	
800	AGGCTTGGAAAGAATTGCAATTGCTTGGGCTACTCATGTACAGATAACCAACTTCTCTGGACACTAAGGGAGACTCTATGTTGGGTGGCTG	
900	TCATCATAGAGAAAAGGGCAAAAGTTGAGGTCACTGACCTCAAAAGAGTTGTGCTGATGGTTCCGGGCTACCCCTGTAACCAGAGT	
1000	DRF6 start	
1000	+1> ***+DRF5 stop	
1100	TTCAAGGGAAACATGGGAGTGGGCTTCAAGATGACTCTGTCATGATGGCTGATGGTTCCGGGCTACCCCTGTAACCAGAGT	
1100	TTCAAGGGAAACATGGGAGTGGGCTTCAAGATGACTCTGTCATGATGGCTGATGGTTCCGGGCTACCCCTGTAACCAGAGT	

FIG. 7A

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TGAATATGCCCTAAAGGTGAGTCGGCCGACTGGCTAAGGCCTTCTGACCTTTGGCTTCAATTGGTACATGACATTTCG
 1200
 GGACTTTCAAGTACAATAAAGGTGGCTCACTATGGAGCAGTAGTGGACTCTTGGGGTGACTCAAGCCATAGAAACCTGGAAATTCACTCACC
 1300
 TCCAGATGCCGTTTGTGCTTGGCTAAGTAACATTCTGGCCCTGCCAACACGTGAAGTGCCTGAGGCTTCAATCCGATTGGGGCAAAATGATA
 1400
 ACCACGCATTGCGTCCGGCTCCACTACGGCAACATTGGTCCCCGGTTAAAAGCCCTCGTGTGGTGGCAGAAAAGCTGTTAA
 1500
 DRF7 start
 +1> ***DRF6 stop
ACAGGGAGTGGTAAACCTTGTTAAATATGCAAATAACCGGCAAGCAGGAGAAAGAAAAATAAGAAGAAAAGAGAAGGGGATGGCAGCTCAATCAGCTGTGCCAGAT
 1600
 GCTGGTAAGATCATCGCTCACCAAAACCAAGTCCAGGGCAAGGGACCCGGAAAGAAAAATAAGAAGAAAACCCGGAGAAGCCCCATTCCCTCTAGCG
 1700
 ACTGAAGATGTCAGACATCACTTACCCCTAGTGAGGTCAATTGTCGTCATTGTCGCTCAATTCCAGACCCCTTTAATCAAGGGCTGGGACTTGGCACCC
 1800
 TGTCAGATTAGGGAGGATAAAGTTACACTGGAGTTAGTTGGCTTACGGCATCATACTGTCGCTGATCCGGTCAACAGGATCACCCCTCAGGATGATG
 1900
 GGCCTGGCATTCGAGGCACTCCAGTGGTGAATTGGAAAGAATGGCTGAATGGCACTGATTAAGTCACCTTCAAGTCAACTTCAAAATTAGGGC
 2000
 GACCGTGGGGTAAAGATTAAATTGGAGAAACACAGGGCGAAAATAAAAAA
 2062

FIG. 7B

FIG. 8

ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	AATGGAGTCG TCGTTAGATC ACTTGTCTA TCATACG GTCACAAA AGGTCCTT -ATGG-GAGG -CTAGAAC ATTTGCAA CGATCTATC GGCCACAAA AGCTCGGCTT	947 14132
ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	CCGTTTCT ATTACCTACA CCCAGCAT GATATAAGC CTAAAGCTGA GTCCCCCG -CCGTTTAGC ATGAACTACA GACTAATT GATATAAGC CTAAAGCTGA CAGGGCGG	1007 14192
ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	ACTGCTAGGC CTTGGACC TTTCGCTT CCTGAATCT GCTTCACTT TCGGTACAT -ACTCTGGGC CTTGGACA TTCTAAATT TCTGAATCT TCGGTACAT	1067 14252
ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GACATTCTGC CACTTCTAGA GTACAAATAA GTCGGCTC ACTATGGAC CAGTAGTGC -GACATATCTGC CATTTCAAT CACCAACCG TCTGGACTT ACCTGGGGG GTGTTCTGG -GCGCTGTT	1127 14311
ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	ACTCTTTCG GCGGCTACT CAGG-CAAACTTGA AAATTGATCAC CTCAGATGC -GCGCTGTT GCGCTGTT CAAGGTCACA GAGTCAGGAA AGTTGATCAC TTCCAGATGC	1185 14370
ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GTTTGTCTGTT TGCTAGGCC CAAGTACATT CTGGCCCTG CCCACCCAG -AGATTGTTGTT GCCTGGCG CGGATACATT CTGGCCCTG CCCATCACG	1245 14430
ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GGAGGTTTC ATCCATTCG GCGAAATGAAACCCAT TTTGCTCG -CCAGGTGTC ATTTAACTCTC AGCTCTGTT AACCCACCAT	1305 14490
ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	TCCACTACG TCAAGGCCAO ATTTGCTCC -CTAACATDAG TCAAGGCCAC TTTGCTCG -TTAACATDAG TCAAGGCCAC TTTGCTCG	1365 14550
ISU 12/7 _a /3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	AAAGCTGTT AAQAGGAGT GTAAACCTT GTTAAATATG COAAATAA -CGAGCTGTT AAQAGGAGT GTTAAACCTC GTTAAACCTC	1413 14598

FIG. 9

Lelystad seq ISU 12/7 ₀ /3' terminal	(14588 – 14974)	A[GGCCGTA AAAACAGA- -----] [CCCACAAATA AAAAGAAAGT A-CAG---C -----] [CCCACAAATA ACAGAACAG ACCAGAACAG	14632
Lelystad seq ISU 12/7 ₀ /3' terminal	(1403 – 1774)	TCCGA[GGG -----] [AATGGCCAG CAGTCATA[CA ACTGTGCCAQ T[GCTGGT]C -----] [MAAGAA[GGG GATGGCAGC CAGTCATA[CA GTGTGCCAG ATGCTGGT]-	1434
Lelystad seq ISU 12/7 ₀ /3' terminal	(14588 – 14974)	C[AATGATAAA -----] [CTCGCA[GGC CAGCAA[TTA CGGG-A -----] [AA-GATCAT CGTCAGAA AACAGTCATA GAGGAA[GGC AdGGG--GA	14681
Lelystad seq ISU 12/7 ₀ /3' terminal	(1403 – 1774)	14728	
Lelystad seq ISU 12/7 ₀ /3' terminal	(14588 – 14974)	A[AGAAAAA- -----] [AGAAAAAA[TA AGAA[AAA -----] [CO[GAGAAC COACATTTC[CC CCTGCTGC -----]	1528
Lelystad seq ISU 12/7 ₀ /3' terminal	(1403 – 1774)	14766	
Lelystad seq ISU 12/7 ₀ /3' terminal	(14588 – 14974)	TGAAGATGAC[-----] [ATCGCCAC[CC AGGTCACCA GACTGA[CC TCCGTTGCT -----] [TGAAGATGAT GTGAGACATC A[TTTACCC[T[AGTGA[CC[CAA[TTGTC -----]	1578
Lelystad seq ISU 12/7 ₀ /3' terminal	(1403 – 1774)	14816	
Lelystad seq ISU 12/7 ₀ /3' terminal	(14588 – 14974)	T[GCAATGAT CCAGACGGT[-----] [TGTGTTAA[CCAGACGGC[T[TAATCAAG CCCGTCGGA[-TGGC[GCT -----] [T[GCAATGAT CCAGACGGC[T[TAATCAAG CCCGTCGGA[T[TCGAA[G-C] -----]	1628
Lelystad seq ISU 12/7 ₀ /3' terminal	(1403 – 1774)	14865	
Lelystad seq ISU 12/7 ₀ /3' terminal	(14588 – 14974)	T[CA[TCAGC [GGCAAGCTCA GTTTCAGG[-----] [TCAGATTCA [GGCAAGCTAA GT]ACACT[G] GGAGTTAGT[-----] [GAGTTATC CTGGCGCTTC -----] [T[GCAATGAT CCAGACGGC[T[TAATCAAG CCCGTCGGA[T[TCGAA[G-C] -----]	1677
Lelystad seq ISU 12/7 ₀ /3' terminal	(1403 – 1774)	14915	
Lelystad seq ISU 12/7 ₀ /3' terminal	(14588 – 14974)	C[TCATACAGT GGGCTGAT[-----] [TCATACAGT GGGCTGAT[-----] [CAGTCACCC[CAGTCACCC[-----] [CAGTCACCC-T CAGTCACCC-T CAG-CA[GA- -----]	14965
Lelystad seq ISU 12/7 ₀ /3' terminal	(1403 – 1774)	14974	
		GCAAGTTAA	1774

FIG. 10

ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	TCGGCTGGCA TTCTTGAGGC ATCCCAGTGT TTGAATTGCA	1814 14976
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AGAA[TGCC]G GTGAA[TGCC]A C[TGAT]TG[GADA] [TTG]TG[CCTCT] TGACAG[TCAG] G[TGAA]AT[GGCC] G[GATT]GG[G] [CTTGCC]CT	1854 15016
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AAGTCACCTA TTCAATTAGG GCGAACCTGT GGGGTAA[GAA] GAGTCACCTA TTCAATTAGG GCGATGACAT GGGGT[DATA]	1800 15056
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	[TTAA][T-]GG CGAGAACAC AC[GCGCAA] TTAAAAAAA CTTAATCAGG CAGGAACCAT GTGACCGAA TTAAAAAAA	1933 15096
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AAAAA AAAAA	1938 15101

FIG. 11

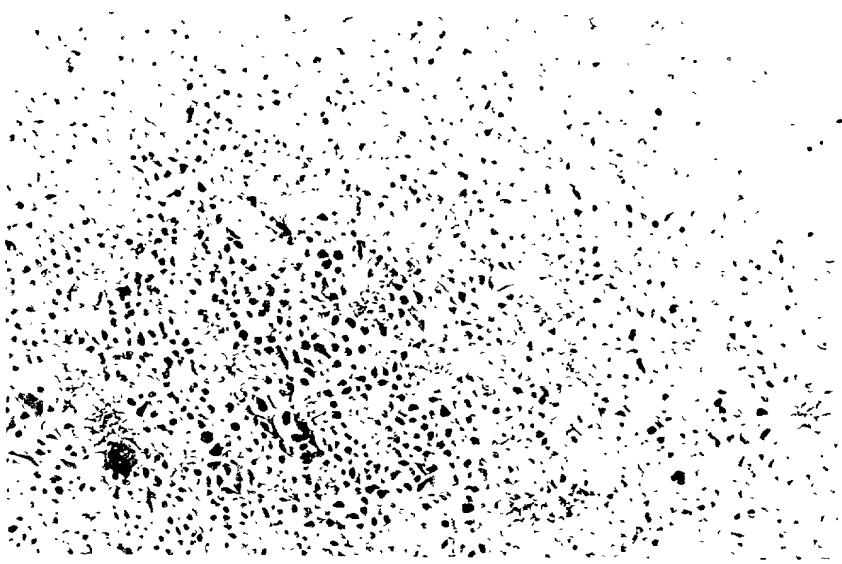


FIG.12

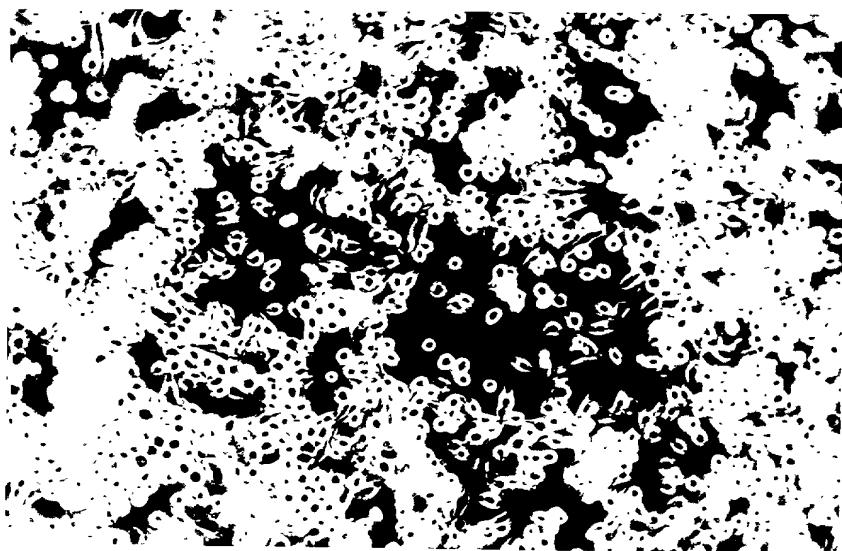


FIG.13

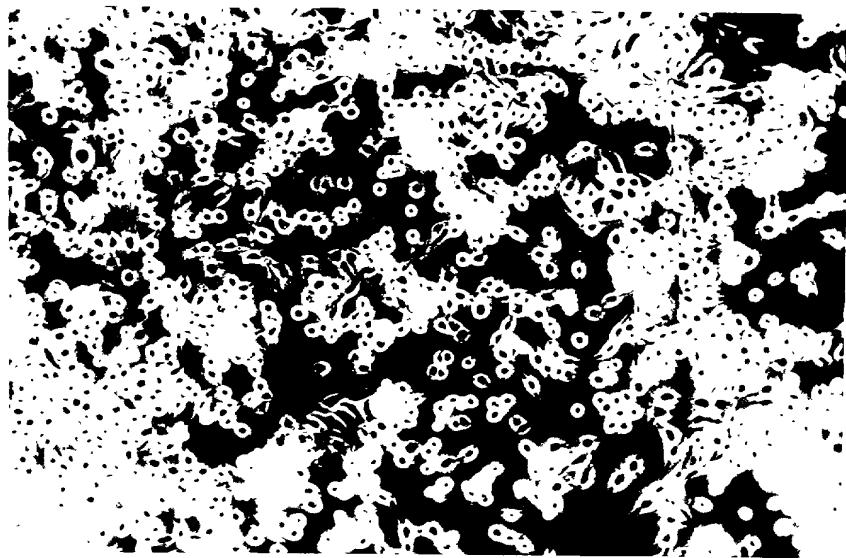


FIG.14

SM E M NP E+M+NP SM

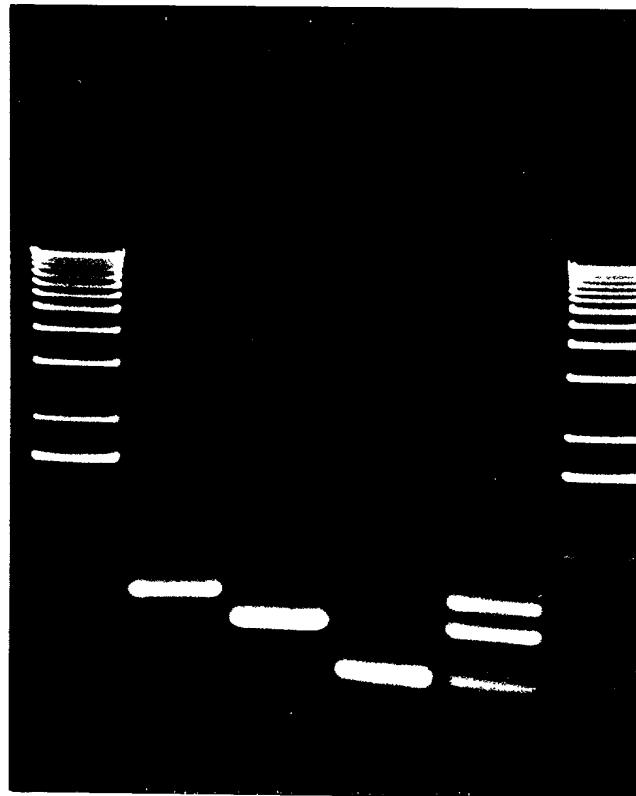


FIG.15

SM pVL1393 E M NP SM

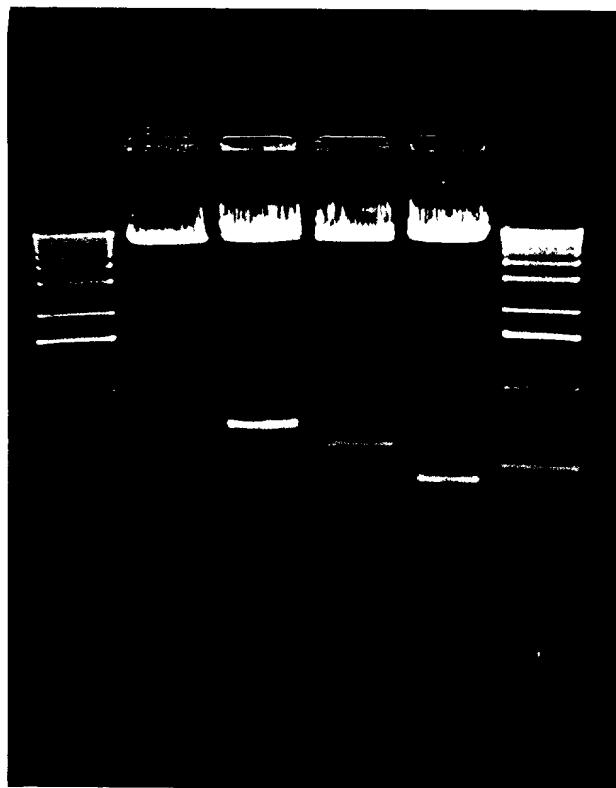


FIG.16

VR 2385 GTTTGTGCTTAGGCCAAGTACATTCTGGCCCTGCCAACACGTTGAAGTGCGCAGGTTTATCCGATTGGCCAATGATAACCACGCATT 398
 ISU-1894 398
 ISU-22 398
 ISU-79 398
 ISU-55 398
 ISU-3927 398
 LV A.....T, GC, T, ., GCGA, T, A, T, TC, C, T, A, GTCA, G, GA, A 395

VR 2385 TGTCTGGGTCCCCGTCACACTACGGTCAACGGCACATTGGTGCCTGGGTAAAGGCTCGTGTGGGGAGAAAGCTGTAAACAGGGAGTG 498
 ISU-1894 498
 ISU-22 T 498
 ISU-79 498
 ISU-55 498
 ISU-3927 498
 LV C, CT, GA, AAAAG, ACTA, AT, A, G, TC, A, A, A, AC, TCGG, C, C, A, CG, G, GA, A, 495

ORF 7 start

+ 1> *** ORF 6 stop
 VR 2385 GTAAACCTTGTAAATAACCCGGCA-AGCAGGAGAAAGAAA-----GGGGATGGCCAGCCAGTCATCAGCTGTG 582
 ISU-1894 C, C, A, - 582
 ISU-22 C, C, A, T, - 582
 ISU-79 C, C, A, - 582
 ISU-55 C, A, - 582
 ISU-3927 A, A, - 582
 LV T, C, C, G, G, CCG, A, A, --, G, --, A, AAGTACAGCTCCGAT, A, C, A, 591

FIG. 17B

With the exception of the first two, all the other species are described from material collected by Mr. J. C. Merriam.

FIG. 17C

VR 2385	CTTGGACC-CCTGTCAGATTCAGGGAGATAAGTTACACTGGGAGTTAGTTGGCTTAGGCATCATACTGTCGGCTGATCCGGTCAAGGATCACCC-	877
ISU-1894A.....	-
ISU-22T.....	-
ISU-79T.....	-
ISU-55T.....	-
ISU-3927	C.....T.....A.....	-
LVGT.....G.....T.....TCCAGC.....A.....G.....C.....TTCAG.....T.....TGG.....GGTTGC.....A.....T.....T.....A.....T.....G	877

			VR	23	85	TCA	G-C	A-----T-GA	***	ORF	7	s-stop
			ISU-1894	,		-----	...	886		
			ISU-22			-----	...	886		
			ISU-79			-----	...	886		
			ISU-55			-----	...	886		
			ISU-3927			-----	...	886		
			LV			C...	T...	GGGTGAAAGT,A.	~~~~~	898		

FIG. 17D

FIG. 18A

VR 2385 DRF6	MESSLDIFCHDSTAPQKVLLAFSITYPVMYALKVSRGRLLGHLVFTLNCAFTFGYMIVHFQSNTNKVALTMGA	VALLWGVSAYETWKFTITSRCR	100
ISU-1894 DRF6	G.....	100
ISU-22 DRF6	G.....	I.....	100
SIU-55 DRF6	G.....	I.....	100
ISU-79 DRF6	G.....Y	I.....	100
ISU-3927 DRF6	G.....N	I.....	100
LV DRF6	G-G.....N.PI.A..LV.....I.....	I.I.....S.....Y.....R.....L.....	99
PRRSV-10 DRF6	G-G.....N.PI.A..LV.....I.....	I.I.....S.....Y.....R.....L.....	99
LDV-C DRF2	G-G.-E..DQTSWY.-IFL.....L.....IA..S..F..T.A.IWNIFI.I..CVS.V.LMYH.-SV..TI..SL..I..V..I..TLVKIVDWLVI..	..	96
LDV-P DRF2	G-G.-E..DQTSWY.-I..I..L..IA..S..F..T.A.IWNIFI.I..CVS.V.LMYH.-SV..T..SL..I..V..I..TLVKIVNWVL..	..	96

VR 2385 DRF6	LCLLGRKYILAPAHHVESAAGFHPIAANDNH-----AFVWRRPGSTTVNGTLVPGLKSLVLGGRKAVKGVVNLVKY-AK	183	
ISU-1894 DRF6	174
ISU-22 DRF6	174
SIU-55 DRF6	174
ISU-79 DRF6	174
ISU-3927 DRF6	R.....K.....	174
LV DRF6	C...R.....L.S.S.SG.R-----,YA.K..L.S.....R.....KR.....R.....	-GR 173	
PRRSV-10 DRF6	C...R.....L.S.S.SG.R-----,YA.K..L.S.....R.....KR.....R.....	-GR 173	
LDV-C DRF2	F...S...PS..D-----TSQGRQSLTTSLTT.....K...L..Q...DFQR.....K...SK.A..L..VS.	171	
LDV-P DRF2	F...S...PS..D-----TSQGRQSLTTSSTT.....K...L..Q...DFQR.....K...SK.A..L..VS.	171	

VR 2385 DRF7 MPNNNTGKQQKRRKK-----GDGQPVNQLCQMLGKIIAHQNQSRGKGPKKKKKNEKPHPLATEDDVRHHTPSERQLCLSSIQTAFNQGAGTCILS 100
 ISU-1894 DRF7 N N Q Q 93
 ISU-22 DRF7 N N Q Q 93
 ISU-79 DRF7 N N Q Q 93
 ISU-3927 DRF7 N K Q Q 1 .. 93
 ISU-55 DRF7 N K Q Q SG 93
 VR2332 DRF7 N TEE Q Q 93
 LV DRF7 ---A N SQ . KKSTAPM N L . AM . KS . R ---QPR . GQA . K A . I . L . QT . S . Q AS . 94
 PRRSV-10 DRF7 ---A N SQ . KKSTAPM N L . AM . KS . R ---QPR . GQA . K A . I . L . QT . S . Q PS . 94
 LDV-C DRF1 SQ . KK . GGQN . ---AN . ---N . LISALLRNAG . --N . K . Q . K . -Q . -L . M . GPS . L . VM . N . V . M . R . LV . L . G . Q . V 85
 LDV-P DRF1 SQ . KK . SGQN . ---AN . ---N . LINALLRNAG . --N . K . Q . K . -Q . -L . M . GPS . L . VM . N . V . M . R . LV . L . G . Q . V 85
 EAV DRF7 ASRRSRP, AASF . ---RN . R --RRQPTSYNDLLRMFG . ---MRVR, PPAQPTQAI, EPGL . DLNQQ . ATLS, NV, RF, MI, H, SL, -A 83
 ~~~~~~  
 LV DRF7 DSGRISYTVEFLPTHHTVRLIRVTASP---SA 134  
 ISU-1894 DRF7 ..... , 123  
 ISU-22 DRF7 ..... , 123  
 ISU-79 DRF7 ..... , 123  
 ISU-3927 DRF7 ..... P . , 123  
 ISU-55 DRF7 ..... , 123  
 VR2332 DRF7 ..... , 123  
 LV DRF7 S . KV . FQ . . M . VA . . . . . STSASQGAS 128  
 PRRSV-10 DRF7 S . KV . FQ . . M . VA . . . . . STSASQGAS 128  
 LDV-C DRF1 G . NF . . S . M . . A . . . . . NAS, NS ----, 115  
 LDV-P DRF1 G . NF . . S . M . . A . . . . . NAS, NS ----, 115  
 EAV DRF7 A . GLT . . SW-V . . KQIQ . KVAPP, G . -----, 110  
 ~~~~

FIG. 18B

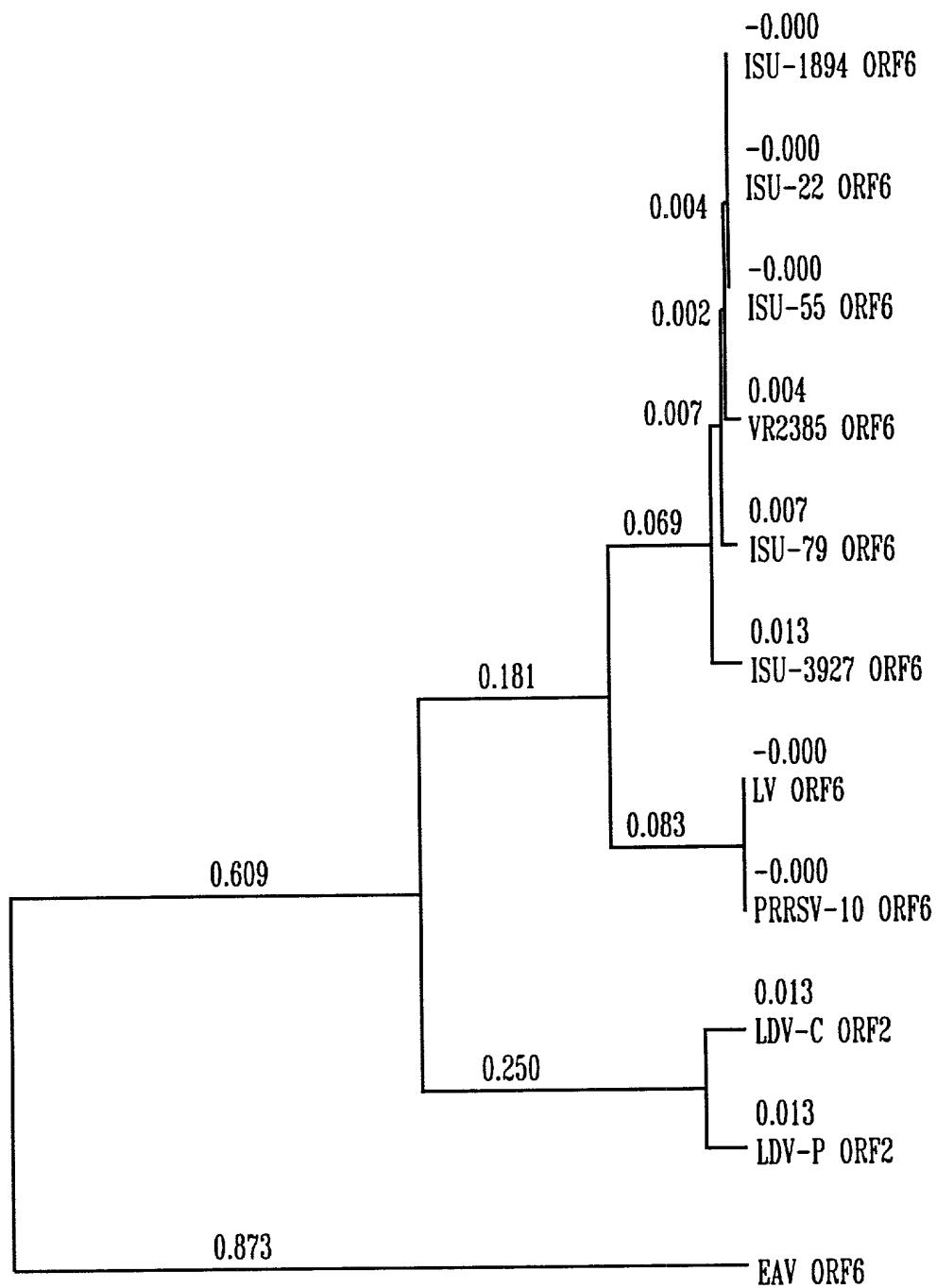


FIG. 19A

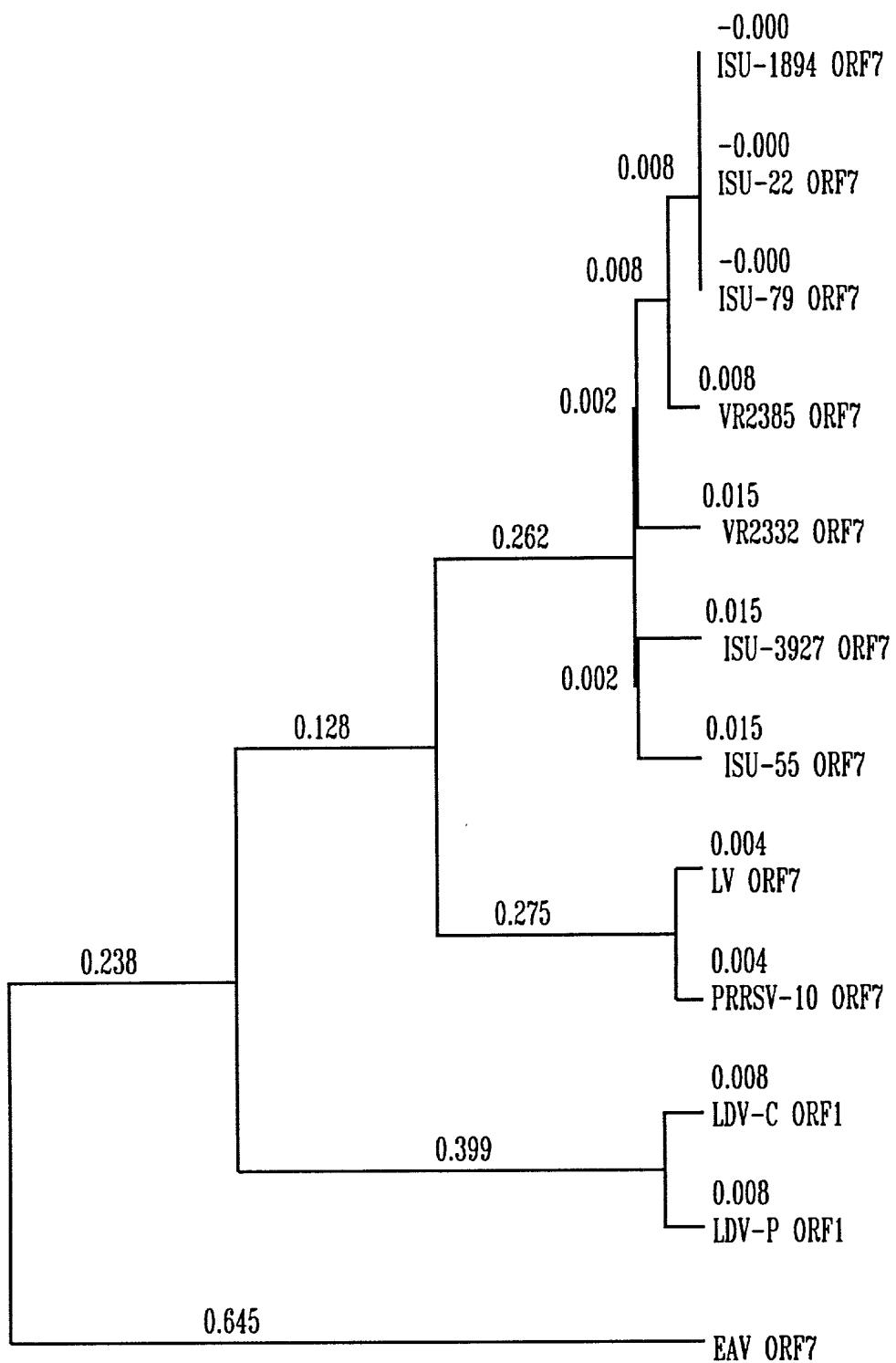


FIG. 19B

start start start start start start
B₁ B₂ B₃ B₄ B₅ B₆ B₇ B₈ B₉ B₁₀ B₁₁

+ Start DRF2
CCTGAATTGAGATGAAATGGGTCTATGCCAAAGCCTTTGACAAAATTGGCCAACTTTTGCACCATTCGGAAAGTTGGCTGGTGGCTTTGCATCAGATTGGTTGCTCCGGATACTCCGTGGCGCC 100
ATCATATAATTTGGCATTTGGTTGGCTTCAACATCGGAAAGTTGGCTGGTGGCTCTCTCAGTGCAGGTGGACATTCCCACCTGGGAACATAAACATCCTTGGGA 200
CTGCCATTCACTCTGAGCAATTACAGAAGAATCCATGAGGCCATTGATGAAATGGTGGCTGGAATGTACCGCATATGGAAAAGCAGGGCTGGCTGGAAACAGGT 300
TGCTTTGGCACCAAAAGGTGTAACCCCTGATTGATGAAATGGTGGCTGGAATGTGGATGGATTTAGTAGCTCGCATCTTGCAGCATCTTGCAGCATTTGAAGCCAGAACCTGTAATAATATCTGGCC 400
AGTGAGCCAGGGCTACGGCTCGCTCGCATTTAGTAGCTGGATGGATTTAGTAGCTCGCATCTTGCAGCATCTTGCAGCATTTGAAGCCAGAACCTGTAATAATATCTGGCC 500
TCTGGCTGCCATGCTACACCAACCTGGCATGACAGGGTCAAATGTAACCAATAGTGTATAATAGTACTTTGAATCAGGTGTTTGCCTGTTTCCCAACCC 600

+ Start DRF3
CTGGTCCGGCAAAAGCTCATGATTCCAGCAATGGCTAAATAGCTGACATTCCCTCTATATTTCCTCTTGTGAGCTCTTGTACTCTTTTGTGT 700

*** Stop DRF2
GGTGGTTGGGTCCAAATGCTACGTACTGTTGGTCCGGCTGGTTAGGGCAATTTCCTCTTGTGAACTCACGGTGAATTACACGGTGTGGCGCC 800
CTTGCTCACCCGGCAAGCAAGCGAGGGCTACGAACCCGGCAGGTGCCCTTGGTGCAGGATAAGGGCATATGTCGATGTGGGAGGACGATCATGATGA 900
ACTAGGGTTGGTGGCTGCCCTCCAGGAAGGCCACTTGACCAAGTGCCTAACGCCCTGGTGGCTGGCTTCAAGCTATACGGCCAGTTC 1000
CATCCGGAGATATTGGGAATTGGGATAGGGATGTTGAGTCAGTCTATGGTGAACATCAAGGACCAATTCAATTTCATGATGGCAGTCAAGAACACCTTGC 1100

FIG. 2OA

5' GATGAGCTTCAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTGTAGGGATTGCCAAAGTCCCTCAGTGCGCACGGGATAGG

+ Start DRF4
CCCCACCATTCAGCCGTGCTTCAGACCTATTACCAAGCATCAGGTGACGGGGCAATTGGTTTACCTAGAATGGGTGGTCCCTCTTTTC 1200
CTCTTGGTTAAATGCTCTTGGTTTCAAGGCCATGTTCAAGTTCAGTTGAGTCTTCAGACATCAAGACATCAAGACCAACACCCGGAG 1300

*** Stop DRF3
CGGCAAGCTTGCCTGGCTCAAGACATCAGTTGCCTTAGGCATCGCAACTCGCAACTCGGCCCTGTAGGGATTGCCAAAGTCCCTCAGTGCGCACGGGATAGG 1400
GACACCCGTATACTACTGTCACAGCCAATGTTACCGATGAGAATTATTGGCATTCTGATCTCTGATCTCATGCTTTCTATGCTCT 1500
GAGATGAGTGAAGGGATTAAAGGTGGTATTGGCAAATGTTGTCAGGCACTGGCAAGTGTGGCAACTTCAACCTTACCAAGTTACGTCCAAACATGTCAAGGAAT 1600
TTACCAACGTTCCCTGGTAGTTGACCATGTCGGCTGCTCCATTCAAGGCCGAGACCATGAGTGGCAACTGTTTAGCTTGCTTTTACCAT 1700

*** Stop DRF4 + Start DRF5
TCATGTCGAATTGAATGTTTAAGTATGTTGGGGAAATGCTGACCGGGCTGTTGCTCGCAATTGGCTTTTATGGTGTATGTCGGCTTGTGT 1799

FIG. 20B

| Consensus | ATGMAATGGGGTCAAGCTTTGAYAAAATYRGCCARCTTGTGAACTGAGAGTCYTGKRWYSRKIGATTAITAIW | 100 |
|--------------|---|-----|
| VR22385 DRF2 | ...A.....TA..CAA.....C.....TG...A..T..T.....T..G.....G.....T..G..GTCCA..T.....CATT..A.. | 100 |
| LV DRF2 | ...C.....AC..TGG..-----T...CA...G..G..C....C..T..TAGTG..G.....TGCC..T.. | 91 |

| | | |
|-----------|---|-----|
| Consensus | YYTKGCCATTWYTGGTGTGAGGWTGGYTRSTGGTCTTYKYMTCAGAKTTGGCTCGGGMTWCTCCGGCCTGCCATTCAAC | 200 |
| VRF2 | TT, G, . . . , TT, C, A, T, C, GG, TGCA, T, A, A, G, C, G, CTTC, G, CT, T, T, T | 200 |
| VRF2 | CC, T, AC, G, A, T, AC, A, T, AC, G, C, T, G, CTTC, G, CT, T, T, T | 191 |

| | | |
|--------------|--|-----|
| Consensus | TCTSMSSAAAYTAYMGAAGRTOCTATIGARGSCTTKYTSYCYMMASTGCMRRSYGGAYAKTCCCACAMTKKGSARYYAARCAYCCWTTGGGKATIGYTTCGGCA | 300 |
| VR22385 DRF2 | GAGC, T, CA, A, G, C, TC, CT, TC, G, CAGGT, C, T, -C, GG, G, ACT, A, T, T, G, C, | 299 |
| IV DRF2 | CCC, C, TC, A, GT, GC, CA, C, AGACC, A, TT, C, GTC, G, C, A, T, T, | 290 |

| | | |
|---------------|---|-----|
| Consensus | CCATRMGAGTKTCMMMCYTGATTGATGARATGGTSTCKCGMATTKACCRSAYCATGGAAWKCAGGWCARGGCTGGCTGGAACARCAGGTTRGTKRGYGA | 400 |
| VR2385 DPF2 | ...AA. - .G. , AAC. C. A. G. , G. A. , G. GC. T. A. AG. A. , G. , T. A. , A. , G. C. , | 398 |
| V VR2385 DPF2 |G. T. , CCA. T. G. C. T. C. T. AG. C. C. TT. T. , A. G. G. , TG. T. , | 386 |

5' T C G A T T C C A G G T C A A T G T R A S S C M T A S W G T A Y A Y A S Y A C K T T G R A Y C R S G T G T K W G C T C R T Y T C C O M A C S C C W G G T W 600

Consensus TSSYSATGCTAMAMMAYCTGYCAYGWYAGGGTCAAATGTRASSCMTASWGTAYAAYASYACKTTGGRAYCRSGTGTKWGCTCRTYTYTCCOMACSCCWGGTW
VR2385 DRF2 GCCCG.....C.CC.C..C...T.AC.....A.G.....A.C.A.GT...T..T.GT..T...A.T.AG...T..T..T..-G..T...A..C..T...T 595
LV DRF2 CGTG.....A.AA.T..-T..-C.TT--,-,-,...G.GC..CA...C..C.CC..G..G.C..GC..-,GA...A.C...C..G..A..A 580

Consensus CSMGGCCMAAGYTKMMYGATTTCMRRCATGGCTMAATGCTCTGTCWIKCWTCTKKTACYYTKTITYRTWGTGCTKTG 700
VR2385 DRF2 CC...A...C.TCAT.....CAG.....A.AGC...A..TT.C..T..A.....T..AG.T...TG..T...TC..T...TG..T...G.. 695
LV DRF2 GA...C...T.GACC.....AGA.....CAG...G..CG.T..C..T.....G..TT.A..GT..CT.G..CA.A....T.. 680

Consensus GYTKCGRRTTCCARYKCTACGYWMGTTTGGTTCCRYTGGYMYRSGGCAAYWTCWTTGARCTSACGGTGA 776
VR2385 DRF2 T.G..GG...ATG...TAC.....GC...TTAGG.....TTTT..T.....A..C..... 771
LV DRF2 C.T..AA.....GCT.....CTA.....AT...CCCAC...CACA..A.....G..G..... 750

FIG. 214. 1

FIG. 21B

| | | |
|-------------|--|-----|
| Consensus | ATGGCTTACATTCGTCAGCTTGTGCTTCTGKGCWKCWTCTTCCCTCTGKGCWKCWTCTKKTACYYTTKTYRITKGRTTCCARYKCTACGYWMGT | 100 |
| LV DRF3 |C..CAG...G..CG.T..C..T.....G..TT.A..GT..CT.G..CA.A.....T..C..T..AA.....GCT.....CTA.... | 100 |
| VR2385 DRF3 |A..AGC..A..TT.C..T..A.....T..AG.T..TG..TC..T..G..T..GG..ATG..TAC.. | 100 |
| Consensus | TTTGGTTTCCRYTGGYMMRSGGAAAYWWTCWTGARCTSACSRSAAYTACACSRRTGCMYGCCYTGGYYACCMGKAAGCRGGCTGCMRARGSCT | 200 |
| LV DRF3 |AT...CCCAC...CACAA..A...G..G..CA.C..C...CA.A..AT...C..TTCT..A..T...G.....CA..A..G.. | 200 |
| VR2385 DRF3 |GC..TTAGG...TTTT..T...A..C..GG..G..T.....GG..G..CC..T..CCTC..C..G...A..-..AG..G..C.. | 199 |
| Consensus | ACGARCCCCGGYGMGKWWCMTKGGTCARRATAGGCATGAYMGRRTGTRGGAGSRYGAYCATGATGARYTAGKKWWGTCSRSTSCCGTCGGSYWCKMCA | 300 |
| LV DRF3 | -...G....TC.TAA..A..G.....AA.....CA.G....A....CGT..C.....GT.-.TTAA...CA.C....C..GTA..GA.. | 298 |
| VR2385 DRF3 | ...A....CA.GTC.C.T....GG.....TC.A...G....GAC..T.....AC...GGTT...-GG..G....T..CCT..TC.. | 298 |
| Consensus | SRGGAMKSMMACTTGACSRGKMTTAYGCCYTGGCTKYYTGTCCCTTWSCTAYRCGGCCARTCCATCCSGAGWRTTCTGGGATAGGGAAITGTGWS | 400 |
| LV DRF3 | A.--CTCAA.....-GG..TA..T..T..T..C...T..TTT.....TTC..CG.....A.....G...T..G.....TC | 395 |
| VR2385 DRF3 | G..AGGCC.....CA..GC..C..C..T...G..CCC.....CAG..TA.....G.....C..A..A.....AG | 398 |
| Consensus | KCGMGTCWYGTKGACAWSMRRCACCARTTCATTGCGYGWKCATGATGGRCASAAYWCMACCKTRYCYMMCSRWSACAACATYTCMGCNKTRYWTSMG | 500 |
| LV DRF3 | G..C...TC..G...AGCGA.....G.....T..C..AG.....A..C..TT..A..G..AT..TAC..GGAC.....C..C..AT..ATA..GC.. | 495 |
| VR2385 DRF3 | T..A...AT..T...TCAAG.....A.....C..T..TT.....G..G..CA..C..T..GC..CCA..CATG.....T..A..GG..GCT..CA.. | 498 |

FIG. 21B. 1

| | | |
|-------------|---|-----|
| Consensus | RCMTATTACASACAYCARRTMGACGGGGCAATTGGTTCAAYTRGAATGGSTGCGKCMYCTTTCYTGGYTGGTKYTMAAYRTMTICWTGGTTTC | 600 |
| LV DRF3 | G, A, C, C, AA, A, | 595 |
| VR2385 DRF3 | A, C, G, T, , GG, C, | 598 |
| Consensus | TSAGGGCGTTGCCCTGAAAGCCMGTGTTCTWSKWCGMRTCTWICAGAYATYRAGACCAACACSAACCGCRGCKGCGGGTTTYRKGTCCCTCARGACATCART | 700 |
| LV DRF3 | G, T, C, TCGA, , CA, , A, T, , TG, | 695 |
| VR2385 DRF3 | C, C, C, A, AGTT, , AG, , T, C, , CA, | 698 |
| Consensus | TGYYTGMGRMTCAAGGSRWCTRGCAAGCKCAWAGAGRMRATTCTCGSAAAGTCGYCCTGCGYCGYCARTRGCGWYRGTAECTCCCAGTAGCATCACGA | 800 |
| LV DRF3 | .. TT, CC, A, C,, GGT, , A,, G, , A, .. AAA,, G,, T, C, , A, T, T, A, C, , TCG, | 795 |
| VR2385 DRF3 | .. CC, TA, G, A, , ---, CAA, .. G, , ---, T, -T, , GCG, ---, ---, C, -C, T, , G, , C, , C, G, , ATA, ----- | 765 |
| Consensus | TAA | 803 |
| LV DRF3 | ... , 798 | |
| VR2385 DRF3 | ---, 765 | |

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| | | |
|-------------|---|-----|
| Consensus | ATGGSTGCKCCMYCTTTTCYCTGGYTGGTKYMAAYRTMTCTGGTTCTSAGGGCTTCCGTGAAGCCMTGTTCTAGAYA | 100 |
| /R2385 DRF4 | ... G... T.. CT..... C.. T... T... TT. A.. TG. C.. T..... C..... C..... C..... C. | 100 |
| V DRF4 | ... C... G.. AC..... T.. C..... C..... GC. C.. CA. A.. A..... G..... T..... C..... T. | 100 |

| | | |
|-------------|--|-----|
| Consensus | TYRAGACCAACACCSACCGCRRGCKGCMGGYTTYRYKGTCCTYCARGACATCARTTGYTYMGRMTCACGGSRWCTCRGGAGCKCAWGAGRMRATTCCCTT | 200 |
| VR2385 DRF4 | .CA.....C.....A..G..A..C..TGCT.....C..A.....G..CC..TA..G..A..---CAA...G..---T..T...GCG..-----. | 189 |
| V DRF4 | .TG.....G..T..C..T..CATG.....T..G.....A..TT..CC..A..G.....GGT...A..G..A..AAA..... | 200 |

| | | |
|--------------|---|-----|
| Consensus | CGAAAGTCGTCYCARTGCGYRMRGCSRTMGGKACWCCSWGTAYATCACKRTMACRGCYAAYGKACCGAYGARIMWTAYTTGAYUMCKCKGAYCTK | 300 |
| VR22385 DRF4 | . C.....-C. T.. G.. C.. CACG .. GA. A.. G.. A.. GT... T.. TG. C.. A.. C.. T.. T.. GAAT.. T.. C.. TTC. T.. T.. T.. T | 288 |
| W DRF 4 | . G.....T.. A.. C.. T.. CA.. C.. T.. GG.. C.. T.. G.. T.. C.. G.. ATCA.. C.. T.. CAA.. G.. G.. C.. G | 300 |

| | | |
|--------------|---|-----|
| Consensus | M, WG, C, K, L, W, L, SL, . . . P, CL, SPSQ, G, WSF, S, WFAPR, SVRALPFTL, NYRRSYE, L, C, D, P, . . . KH | 100 |
| LV DRF2, | . Q, . H, GV, SASCSWTPS, SSLLV, LI, ---, PF, . ---, Y, . G, . . . D, Y, . F, E, . . . F, P, GL, PN, RP, V, QFAV, . | 90 |
| VR2385 DRF2, | K, . L, --, ---AFLTK, AN-FL, MLSRSSWCP, LI, . YFW, F, A, . . . V, W, . A, D, S, AF, SQ, QV, I, TWGT, . | 93 |

| | | |
|--------------|---|-----|
| Consensus | PLGM, WH, VS, LIDEMVSRR, Y, . ME, GQAAWKQVV, EATL, . . . S, LD, V, HFQHLAA, EA, C, . L, SRL, ML, . L, NW, . . . YN, TL, . V, . . . | 200 |
| LV DRF2, | F, . MR, . H, I, QT, . HS, G, TKL, G, . I, T, V, . DS, RF, S, . . . V, . KN, AV--G, . SLQ, . T, . DR, ELI | 188 |
| VR2385 DRF2, | L, . HK, . T, M, RI, . KA, S, SRI, S, . V, A, I, . ET, KY, A, . . . P, . HH, RMIGS, . TIV, . S, . NQ, FAV | 193 |

| | | |
|--------------|--|-----|
| Consensus | FPTPG, RPKL, DF, QWLI, VH, SIFSSVA, S, TLF, VLWLR, P, LR, VFGF, W, A, | 264 |
| LV DRF2, | T, . . . R, . . . S, . A, S, V, . . . I, I, A, Y, . . . H, PT, ---THISS | 249 |
| VR2385 DRF2, | S, . . . H, . Q, . . . A, . S, A, C, V, V, M, . T, . . . R, LG, IFLSNSR- | 257 |

MA., C., FLC., Y., A., S., T., GFWFPL., GN, SFELT, NYT, C, PC, T, QAA., EPGR, MC, IGHIRC, E, DHDIEL., PSSG., HQ, ARFHf., GFIC, LVHS, LASN, SS, L., AH, T., I., I.M., S, S., RQRL., NM, K., E, R., LMSI., YDN, 100

Consensus MA., C., FLC., Y., A., S., T., GFWFPL., GN, SFELT, NYT, C, PC, T, QAA., EPGR, MC, IGHIRC, E, DHDIEL., PSSG., HQ, ARFHf., GFIC, LVHS, LASN, SS, L., AH, T., I., I.M., S, S., RQRL., NM, K., E, R., LMSI., YDN, 100
LV DRF3., VR2385 DRF3.

Consensus ...L., YAWLA, LSFSY, AQFHPE, FGIGNVSRV, VD, HQFICA, HDG, N, T., NISA., YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL, 200
LV DRF3., VR2385 DRF3.

Consensus RRSP, S, VS, R, Q, RPT, P, S, TS, L, R, F, K, S., 266
LV DRF3., VR2385 DRF3.

FIG. 22B

Consensus M, A, LF, L, G., VS, AFACKPCFS, LSDI, TNTAAAGF, VLQDI, C, R., A, E, I., K, QCR, A, GTP, YIT, TANVTDE, YL, , DL, 100
LV DRF4., VR2385 DRF3.

Consensus LMLS, CLFYASEMSEKGFKV, FGNWSG, V, CVNFT, YV, HW, TQ, V, RLLHF, TP, MRWAT, ACLF, ILLAI, 184
LV DRF4., VR2385 DRF4.

FIG. 22C



FIG.23

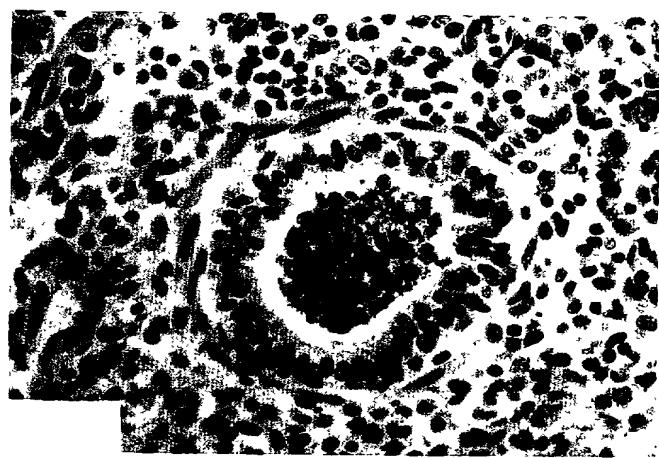


FIG.24

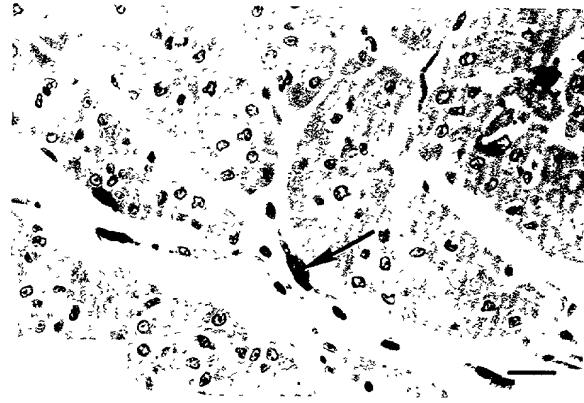


FIG.25

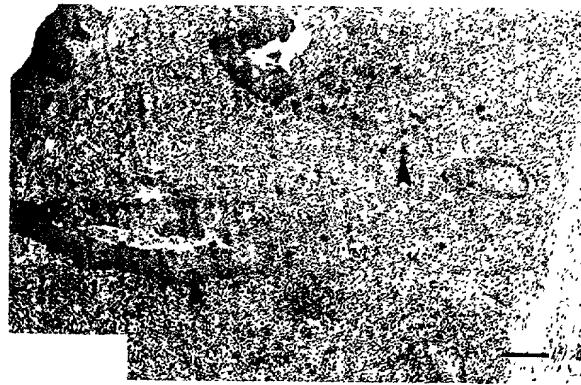


FIG.26

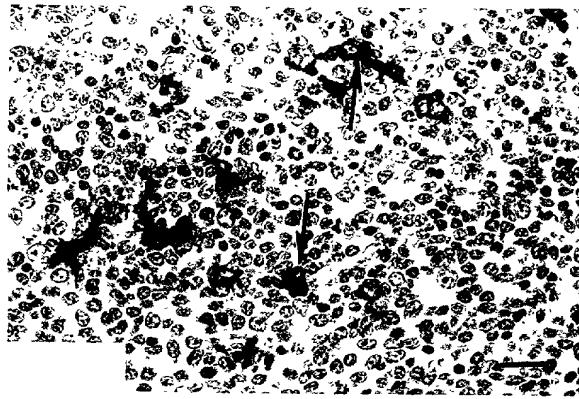


FIG.27



FIG.28A



FIG.28B



FIG.28C

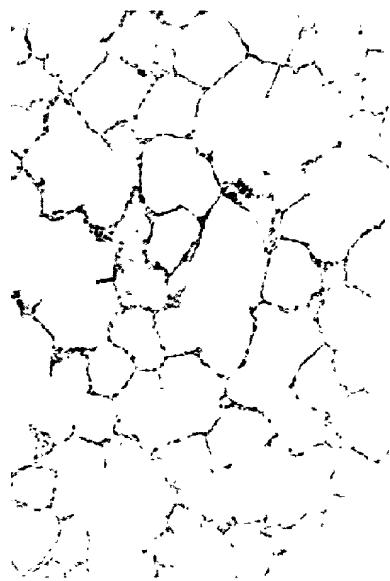


FIG.29A



FIG.29B

FIG.29C

FIG.30A

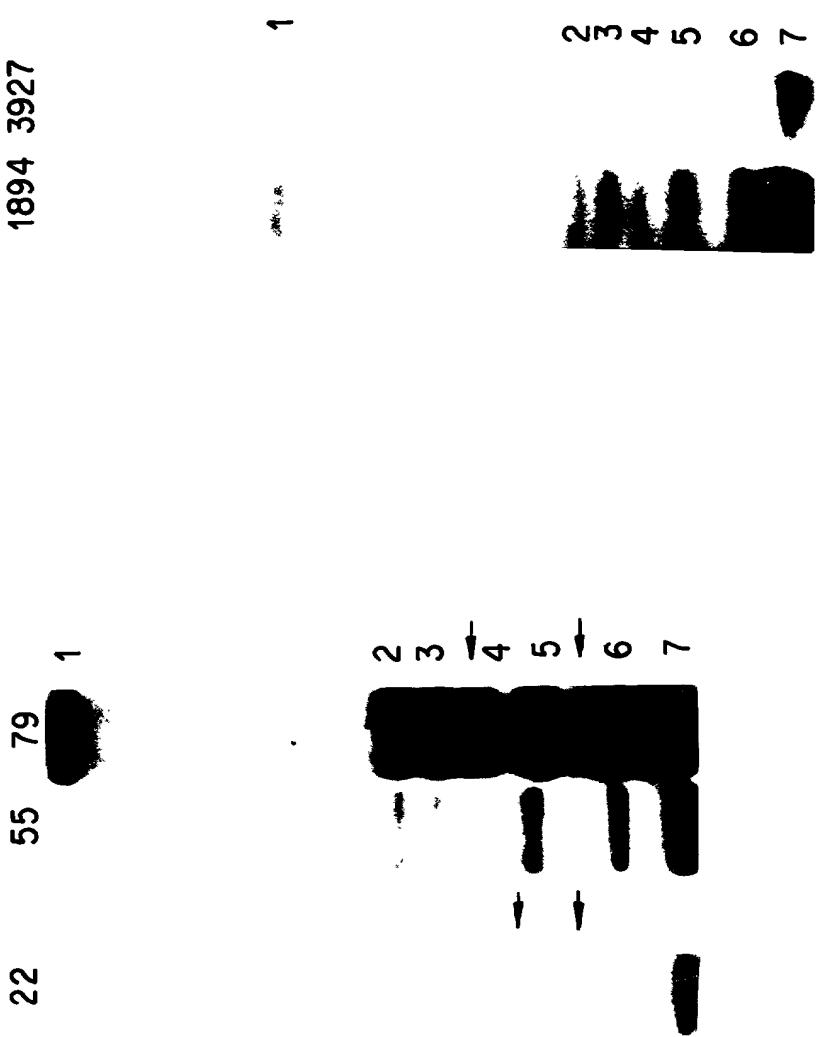


FIG.30B

